

Figure 1:
WWP1 open reading frame and translation to corresponding polypeptide

	1	ATG	GCC	ACT	GCT	TCA	CCA	AGG	TCT	GAT	ACT	AGT	AAT	AAC	CAC	AGT	45
5	1	M	A	T	A	S	P	R	S	D	T	S	N	N	H	S	15
	46	GGA	AGG	TTG	CAG	TTA	CAG	GTA	ACT	GTT	TCT	AGT	GCC	AAA	CTT	AAA	90
	16	G	R	L	Q	L	Q	V	T	V	S	S	A	K	L	K	30
10	91	AGA	AAA	AAG	AAC	TGG	TTC	GGA	ACA	GCA	ATA	TAT	ACA	GAA	GTA	GTT	135
	31	R	K	K	N	W	F	G	T	A	I	Y	T	E	V	V	45
	136	GTA	GAT	GGA	GAA	ATT	ACG	AAA	ACA	GCA	AAA	TCC	AGT	AGT	TCT	TCT	180
15	46	V	D	G	E	I	T	K	T	A	K	S	S	S	S	S	60
	181	AAT	CCA	AAA	TGG	GAT	GAA	CAG	CTA	ACT	GTA	AAT	GTT	ACG	CCA	CAG	225
	61	N	P	K	W	D	E	Q	L	T	V	N	V	T	P	Q	75
	226	ACT	ACA	TTG	GAA	TTT	CAA	GTT	TGG	AGC	CAT	CGC	ACT	TTA	AAA	GCA	270
20	76	T	T	L	E	F	Q	V	W	S	H	R	T	L	K	A	90
	271	GAT	GCT	TTA	TTA	GGA	AAA	GCA	ACG	ATA	GAT	TTG	AAA	CAA	GCT	CTG	315
	91	D	A	L	L	G	K	A	T	I	D	L	K	Q	A	L	105
25	316	TTG	ATA	CAC	AAT	AGA	AAA	TTG	GAA	AGA	GTG	AAA	GAA	CAA	TTA	AAA	360
	106	L	I	H	N	R	K	L	E	R	V	K	E	Q	L	K	120
	361	CTT	TCC	TTG	GAA	AAC	AAG	AAT	GGC	ATA	GCA	CAA	ACT	GGT	GAA	TTG	405
30	121	L	S	L	E	N	K	N	G	I	A	Q	T	G	E	L	135
	406	ACA	GTT	GTG	CTT	GAT	GGA	TTG	GTG	ATT	GAG	CAA	GAA	AAT	ATA	ACA	450
	136	T	V	V	L	D	G	L	V	I	E	Q	E	N	I	T	150
	451	AAC	TGC	AGC	TCA	TCT	CCA	ACC	ATA	GAA	ATA	CAG	GAA	AAT	GGT	GAT	495
35	151	N	C	S	S	S	P	T	I	E	I	Q	E	N	G	D	165
	496	GCC	TTA	CAT	GAA	AAT	GGA	GAG	CCT	TCA	GCA	AGG	ACA	ACT	GCC	AGG	540
	166	A	L	H	E	N	G	E	P	S	A	R	T	T	A	R	180
40	541	TTG	GCT	GTT	GAA	GGC	ACG	AAT	GGA	ATA	GAT	AAT	CAT	GTA	CCT	ACA	585
	181	L	A	V	E	G	T	N	G	I	D	N	H	V	P	T	195
	586	AGC	ACT	CTA	GTC	CAA	AAC	TCA	TGC	TGC	TCG	TAT	GTA	GTT	AAT	GGA	630
45	196	S	T	L	V	Q	N	S	C	C	S	Y	V	V	N	G	210
	631	GAC	AAC	ACA	CCT	TCA	TCT	CCG	TCT	CAG	GTT	GCT	GCC	AGA	CCC	AAA	675
	211	D	N	T	P	S	S	P	S	Q	V	A	A	R	P	K	225
	676	AAT	ACA	CCA	GCT	CCA	AAA	CCA	CTC	GCA	TCT	GAG	CCT	GCC	GAT	GAC	720
50	226	N	T	P	A	P	K	P	L	A	S	E	P	A	D	D	240
	721	ACT	GTT	AAT	GGA	GAA	TCA	TCC	TCA	TTT	GCA	CCA	ACT	GAT	AAT	GCG	765
	241	T	V	N	G	E	S	S	S	F	A	P	T	D	N	A	255
55	766	TCT	GTC	ACG	GGT	ACT	CCA	GTA	GTG	TCT	GAA	GAA	AAT	GCC	TTG	TCT	810
	256	S	V	T	G	T	P	V	V	S	E	E	N	A	L	S	270
	811	CCA	AAT	TGC	ACT	AGT	ACT	ACT	GTT	GAA	GAT	CCT	CCA	GTT	CAA	GAA	855
60	271	P	N	C	T	S	T	T	V	E	D	P	P	V	Q	E	285
	856	ATA	CTG	ACT	TCC	TCA	GAA	AAC	AAT	GAA	TGT	ATT	CCT	TCT	ACC	AGT	900
	286	I	L	T	S	S	E	N	N	E	C	I	P	S	T	S	300
	901	GCA	GAA	TTG	GAA	TCT	GAA	GCT	AGA	AGT	ATA	TTA	GAG	CCT	GAC	ACC	945

	301	A	E	L	E	S	E	A	R	S	I	L	E	P	D	T	315
	946	TCT	AAT	TCT	AGA	AGT	AGT	TCT	GCT	TTT	GAA	GCA	GCC	AAA	TCA	AGA	990
5	316	S	N	S	R	S	S	S	A	F	E	A	A	K	S	R	330
	991	CAG	CCA	GAT	GGG	TGT	ATG	GAT	CCT	GTA	CGG	CAG	CAG	TCT	GGG	AAT	1035
	331	Q	P	D	G	C	M	D	P	V	R	Q	Q	S	G	N	345
10	1036	GCC	AAC	ACA	GAA	ACC	TTG	CCA	TCA	GGG	TGG	GAA	CAA	AGA	AAA	GAT	1080
	346	A	N	T	E	T	L	P	S	G	W	E	Q	R	K	D	360
	1081	CCT	CAT	GGT	AGA	ACC	TAT	TAT	GTG	GAT	CAT	AAT	ACT	CGA	ACT	ACC	1125
	361	P	H	G	R	T	Y	Y	V	D	H	N	T	R	T	T	375
15	1126	ACA	TGG	GAG	AGA	CCA	CAA	CCT	TTA	CCT	CCA	GGT	TGG	GAA	AGA	AGA	1170
	376	T	W	E	R	P	Q	P	L	P	P	G	W	E	R	R	390
	1171	GTT	GAT	GAT	CGT	AGA	AGA	GTT	TAT	TAT	GTG	GAT	CAT	AAC	ACC	AGA	1215
20	391	V	D	D	R	R	R	V	Y	Y	V	D	H	N	T	R	405
	1216	ACA	ACA	ACG	TGG	CAG	CGG	CCT	ACC	ATG	GAA	TCT	GTC	CGA	AAT	TTT	1260
	406	T	T	T	W	Q	R	P	T	M	E	S	V	R	N	F	420
25	1261	GAA	CAG	TGG	CAA	TCT	CAG	CGG	AAC	CAA	TTG	CAG	GGA	GCT	ATG	CAA	1305
	421	E	Q	W	Q	S	Q	R	N	Q	L	Q	G	A	M	Q	435
	1306	CAG	TTT	AAC	CAA	CGA	TAC	CTC	TAT	TCG	GCT	TCA	ATG	TTA	GCT	GCA	1350
	436	Q	F	N	Q	R	Y	L	Y	S	A	S	M	L	A	A	450
30	1351	GAA	AAT	GAC	CCT	TAT	GGA	CCT	TTG	CCA	CCA	GGC	TGG	GAA	AAA	AGA	1395
	451	E	N	D	P	Y	G	P	L	P	P	G	W	E	K	R	465
	1396	GTG	GAT	TCA	ACA	GAC	AGG	GTT	TAC	TTT	GTG	AAT	CAT	AAC	ACA	AAA	1440
35	466	V	D	S	T	D	R	V	Y	F	V	N	H	N	T	K	480
	1441	ACA	ACC	CAG	TGG	GAA	GAT	CCA	AGA	ACT	CAA	GGC	TTA	CAG	AAT	GAA	1485
	481	T	T	Q	W	E	D	P	R	T	Q	G	L	Q	N	E	495
40	1486	GAA	CCC	CTG	CCA	GAA	GGC	TGG	GAA	ATT	AGA	TAT	ACT	CGT	GAA	GGT	1530
	496	E	P	L	P	E	G	W	E	I	R	Y	T	R	E	G	510
	1531	GTA	AGG	TAC	TTT	GTT	GAT	CAT	AAC	ACA	AGA	ACA	ACA	ACA	TTC	AAA	1575
	511	V	R	Y	F	V	D	H	N	T	R	T	T	T	F	K	525
45	1576	GAT	CCT	CGC	AAT	GGG	AAG	TCA	TCT	GTA	ACT	AAA	GGT	GGT	CCA	CAA	1620
	526	D	P	R	N	G	K	S	S	V	T	K	G	G	P	Q	540
50	1621	ATT	GCT	TAT	GAA	CGC	GGC	TTT	AGG	TGG	AAG	CTT	GCT	CAC	TTC	CGT	1665
	541	I	A	Y	E	R	G	F	R	W	K	L	A	H	F	R	555
	1666	TAT	TTG	TGC	CAG	TCT	AAT	GCA	CTA	CCT	AGT	CAT	GTA	AAG	ATC	AAT	1710
	556	Y	L	C	Q	S	N	A	L	P	S	H	V	K	I	N	570
55	1711	GTG	TCC	CGG	CAG	ACA	TTG	TTT	GAA	GAT	TCC	TTC	CAA	CAG	ATT	ATG	1755
	571	V	S	R	Q	T	L	F	E	D	S	F	Q	Q	I	M	585
	1756	GCA	TTA	AAA	CCC	TAT	GAC	TTG	AGG	AGG	CGC	TTA	TAT	GTA	ATA	TTT	1800
	586	A	L	K	P	Y	D	L	R	R	R	L	Y	V	I	F	600
60	1801	AGA	GGA	GAA	GAA	GGA	CTT	GAT	TAT	GGT	GGC	CTA	GCG	AGA	GAA	TGG	1845
	601	R	G	E	E	G	L	D	Y	G	G	L	A	R	E	W	615
65	1846	TTT	TTC	TTG	CTT	TCA	CAT	GAA	GTT	TTG	AAC	CCA	ATG	TAT	TGC	TTA	1890
	616	F	F	L	L	S	H	E	V	L	N	P	M	Y	C	L	630

	1891	TTT	GAG	TAT	GCG	GGC	AAG	AAC	AAC	TAT	TGT	CTG	CAG	ATA	AAT	CCA	1935
	631	F	E	Y	A	G	K	N	N	Y	C	L	Q	I	N	P	645
5	1936	GCA	TCA	ACC	ATT	AAT	CCA	GAC	CAT	CTT	TCA	TAC	TTC	TGT	TTC	ATT	1980
	646	A	S	T	I	N	P	D	H	L	S	Y	F	C	F	I	660
	1981	GGT	CGT	TTT	ATT	GCC	ATG	GCA	CTA	TTT	CAT	GGA	AAG	TTT	ATC	GAT	2025
	661	G	R	F	I	A	M	A	L	F	H	G	K	F	I	D	675
10	2026	ACT	GGT	TTC	TCT	TTA	CCA	TTC	TAC	AAG	CGT	ATG	TTA	AGT	AAA	AAA	2070
	676	T	G	F	S	L	P	F	Y	K	R	M	L	S	K	K	690
	2071	CTT	ACT	ATT	AAG	GAT	TTG	GAA	TCT	ATT	GAT	ACT	GAA	TTT	TAT	AAC	2115
	691	L	T	I	K	D	L	E	S	I	D	T	E	F	Y	N	705
15	2116	TCC	CTT	ATC	TGG	ATA	AGA	GAT	AAC	AAC	ATT	GAA	GAA	TGT	GGC	TTA	2160
	706	S	L	I	W	I	R	D	N	N	I	E	E	C	G	L	720
	2161	GAA	ATG	TAC	TTT	TCT	GTT	GAC	ATG	GAG	ATT	TTG	GGA	AAA	GTT	ACT	2205
20	721	E	M	Y	F	S	V	D	M	E	I	L	G	K	V	T	735
	2206	TCA	CAT	GAC	CTG	AAG	TTG	GGA	GGT	TCC	AAT	ATT	CTG	GTG	ACT	GAG	2250
	736	S	H	D	L	K	L	G	G	S	N	I	L	V	T	E	750
25	2251	GAG	AAC	AAA	GAT	GAA	TAT	ATT	GGT	TTA	ATG	ACA	GAA	TGG	CGT	TTT	2295
	751	E	N	K	D	E	Y	I	G	L	M	T	E	W	R	F	765
	2296	TCT	CGA	GGA	GTA	CAA	GAA	CAG	ACC	AAA	GCT	TTC	CTT	GAT	GGT	TTT	2340
	766	S	R	G	V	Q	E	Q	T	K	A	F	L	D	G	F	780
30	2341	AAT	GAA	GTT	GTT	CCT	CTT	CAG	TGG	CTA	CAG	TAC	TTC	GAT	GAA	AAA	2385
	781	N	E	V	V	P	L	Q	W	L	Q	Y	F	D	E	K	795
	2386	GAA	TTA	GAG	GTT	ATG	TTG	TGT	GGC	ATG	CAG	GAG	GTT	GAC	TTG	GCA	2430
35	796	E	L	E	V	M	L	C	G	M	Q	E	V	D	L	A	810
	2431	GAT	TGG	CAG	AGA	AAT	ACT	GTT	TAT	CGA	CAT	TAT	ACA	AGA	AAC	AGC	2475
	811	D	W	Q	R	N	T	V	Y	R	H	Y	T	R	N	S	825
40	2476	AAG	CAA	ATC	ATT	TGG	TTT	TGG	CAG	TTT	GTG	AAA	GAG	ACA	GAC	AAT	2520
	826	K	Q	I	I	W	F	W	Q	F	V	K	E	T	D	N	840
	2521	GAA	GTA	AGA	ATG	CGA	CTA	TTG	CAG	TTC	GTC	ACT	GGA	ACC	TGC	CGT	2565
45	841	E	V	R	M	R	L	L	Q	F	V	T	G	T	C	R	855
	2566	TTA	CCT	CTA	GGA	GGA	TTT	GCT	GAG	CTC	ATG	GGA	AGT	AAT	GGG	CCT	2610
	856	L	P	L	G	G	F	A	E	L	M	G	S	N	G	P	870
	2611	CAA	AAG	TTT	TGC	ATT	GAA	AAA	GTT	GGC	AAA	GAC	ACT	TGG	TTA	CCA	2655
50	871	Q	K	F	C	I	E	K	V	G	K	D	T	W	L	P	885
	2656	AGA	AGC	CAT	ACA	TGT	TTT	AAT	CGC	TTG	GAT	CTA	CCA	CCA	TAT	AAG	2700
	886	R	S	H	T	C	F	N	R	L	D	L	P	P	Y	K	900
55	2701	AGT	TAT	GAA	CAA	CTA	AAG	GAA	AAA	CTT	CTT	TTT	GCA	ATA	GAA	GAG	2745
	901	S	Y	E	Q	L	K	E	K	L	L	F	A	I	E	E	915
	2746	ACA	GAG	GGA	TTT	GGA	CAA	GAA	GAT	TAC	AAG	GAC	GAC	GAC	GAT	AAG	2790
60	916	T	E	G	F	G	Q	E	D	Y	K	D	D	D	D	K	930
	2791	TGA															2793
	931	*															

Figure 2:
WWP1 antisense fragment

CCGCCGCGTTNTAAGCATTTGTGGACCCCTTTAGTNCAGATGACTTCCCATTGCGAGGATCTTTGAATGTTG
5 TTGTTCTTGTGTTATGATCAACAAAGTACCTTACACCTTCACGAGTATATCTAATTTCCCAGCCTTCTGGCA
GGGGTTCTTCATTCTGTAAGCCTTGAGTTCTTGGATCTTCCCACTGGGTGTTTTTGTGTTATGATTCACAA
AGTAAACCCTGTCTGTTGAATCCACTCTTTTTTCCCAGCCTGGTGGCAAAGGTCCATAAGGGTCATTTTCTG
CAGCTAACATTGAAGCCGAATAGAGGTATCGTTGGTTAACTGTTGCATAGCTCCCTGCAATTGGTTCGCT
GAGATTGCCACTGNTCAAAATTNCGGACAGATTCATGGTAGGCCGCTGCCACGTTGTTGTTCTGGTGTAT
10 GATCCACATAATAAACTCCTCTACGATCATCAACTCTCTTTCCCAACCTGGAGGTAAAGGTTGTGGTCTCT
CCCATGTGGTAGTTTCGAGCATTATGANCCACATAATACGCTCTACCATGAGGATCTTTTCTTGTGCCACC
CCTGATGGCAANGNTTCTGTGTTGGCATTCCCAGACTGCTGCCGNACA

Figure 3:
Alignment between the WWP1 open reading frame and the WWP1 antisense fragment of Figure 2

5	WWP1 ORF	1	ATGGCCACTGCTTCACCAAGGTCTGATACTAGTAATAACCACAGTGGAGGTTGCAGTTA
	WWP1 AS	1	-----
	WWP1 ORF	61	CAGGTAAC TGTTC TAGTGCCAACTTAAAAGAAAAAGAACTGGTTCGGAACAGCAATA
	WWP1 AS	1	-----
10	WWP1 ORF	121	TATACAGAAGTAGTTGTAGATGGAGAAATTACGAAAACAGCAAAATCCAGTAGTTCTTCT
	WWP1 AS	1	-----
	WWP1 ORF	181	AATCCAAAATGGGATGAACAGCTAACTGTAAATGTTACGCCACAGACTACATTGGAATTT
15	WWP1 AS	1	-----
	WWP1 ORF	241	CAAGTTTGGAGCCATCGCACTTTAAAAGCAGATGCTTTATTAGGAAAAGCAACGATAGAT
	WWP1 AS	1	-----
20	WWP1 ORF	301	TTGAAACAAGCTCTGTTGATACACAATAGAAAATTGGAAAGAGTGAAAGAACAAATTAATA
	WWP1 AS	1	-----
	WWP1 ORF	361	CTTTCCTTGGAAAACAAGAATGGCATAGCACAACTGGTGAATTGACAGTTGTGCTTGAT
	WWP1 AS	1	-----
25	WWP1 ORF	421	GGATTGGTGATTGAGCAAGAAAATATAACAACTGCAGCTCATCTCCAACCATAGAAATA
	WWP1 AS	1	-----
	WWP1 ORF	481	CAGGAAAATGGTGATGCCTTACATGAAAATGGAGAGCCTTCAGCAAGGACAACTGCCAGG
30	WWP1 AS	1	-----
	WWP1 ORF	541	TTGGCTGTTGAAGGCACGAATGGAATAGATAATCATGTACCTACAAGCACTCTAGTCCAA
	WWP1 AS	1	-----
35	WWP1 ORF	601	AACTCATGCTGCTCGTATGTAGTTAATGGAGACAACACACCTTCATCTCCGTCTCAGGTT
	WWP1 AS	1	-----
	WWP1 ORF	661	GCTGCCAGACCCAAAAATACACCAGCTCCAAAACCACTCGCATCTGAGCCTGCCGATGAC
	WWP1 AS	1	-----
40	WWP1 ORF	721	ACTGTTAATGGAGAATCATCCTCATTTCACCAACTGATAATGCGTCTGTACGGGTACT
	WWP1 AS	1	-----
	WWP1 ORF	781	CCAGTAGTGTCTGAAGAAAATGCCTTGTCTCCAAATTGCACTAGTACTACTGTTGAAGAT
45	WWP1 AS	1	-----
	WWP1 ORF	841	CCTCCAGTTCAAGAAATACTGACTTCCTCAGAAAACAATGAATGTATTCTTCTACCACT
	WWP1 AS	1	-----
50	WWP1 ORF	901	GCAGAATTGGAATCTGAAGCTAGAAGTATATTAGAGCCTGACACCTCTAATTCTAGAAGT
	WWP1 AS	1	-----
	WWP1 ORF	961	AGTTCTGCTTTTGAAGCAGCCAAATCAAGACAGCCAGATGGGTGTATGGATCCTGTACGG
	WWP1 AS	1	-----TGTNCGG
55	WWP1 ORF	1021	CAGCAGTCTGGGAATGCCAACACAGAAACCTTGCCATCA-GGGTGGGAACAAAGAAAAGA
	WWP1 AS	8	CAGCAGTCTGGGAATGCCAACACAGAAACNTTGCCATCAGGGTGGGAACAAAGAAAAGA
	WWP1 ORF	1080	TCCTCATGGTAGAACCATTATGTGGATCATAATACTCGAACTACCACATGGGAGAGACC
60	WWP1 AS	68	TCCTCATGGTAGAGCGTATTATGTGGNTCATAATGCTCGAACTACCACATGGGAGAGACC
	WWP1 ORF	1140	ACAACCTTTACCTCCAGGTTGGGAAAGAAGAGTTGATGATCGTAGAAGAGTTTATTATGT
	WWP1 AS	128	ACAACCTTTACCTCCAGGTTGGGAAAGAAGAGTTGATGATCGTAGAAGAGTTTATTATGT

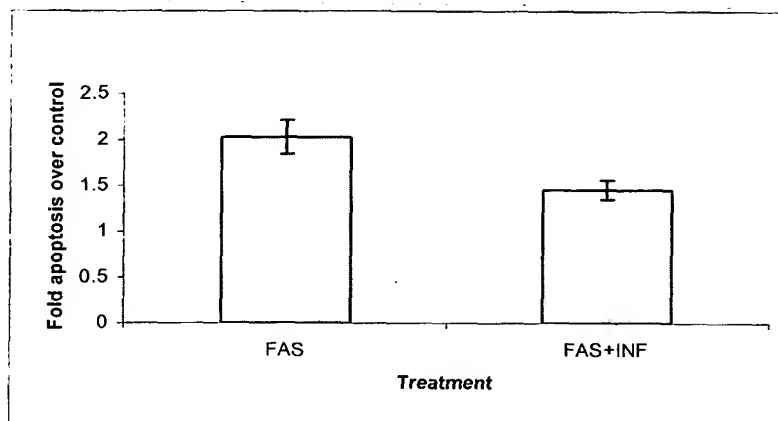
	WWP1 ORF	1200	GGATCATAACACCAGAACAACAACGTGGCAGCGGCCTACCATGGAATCTGTCCGAAATTT
	WWP1 AS	188	GGATCATAACACCAGAACAACAACGTGGCAGCGGCCTACCATGGAATCTGTCCGNAATTT
5	WWP1 ORF	1260	TGAACAGTGGCAATCTCAGCGGAACCAATTGCAGGGAGCTATGCAACAGTTTAACCAACG
	WWP1 AS	248	TGANCAGTGGCAATCTCAGCGGAACCAATTGCAGGGAGCTATGCAACAGTTTAACCAACG
	WWP1 ORF	1320	ATACCTCTATTTCGGCTTCAATGTTAGCTGCAGAAAATGACCCTTATGGACCTTTGCCACC
10	WWP1 AS	308	ATACCTCTATTTCGGCTTCAATGTTAGCTGCAGAAAATGACCCTTATGGACCTTTGCCACC
	WWP1 ORF	1380	AGGCTGGGAAAAAGAGTGGATTCAACAGACAGGGTTTACTTTGTGAATCATAACACAAA
	WWP1 AS	368	AGGCTGGGAAAAAGAGTGGATTCAACAGACAGGGTTTACTTTGTGAATCATAACACAAA
	WWP1 ORF	1440	AACAACCCAGTGGGAAGATCCAAGAACTCAAGGCTTACAGAATGAAGAACCCCTGCCAGA
15	WWP1 AS	428	AACAACCCAGTGGGAAGATCCAAGAACTCAAGGCTTACAGAATGAAGAACCCCTGCCAGA
	WWP1 ORF	1500	AGGCTGGGAAATTAGATATACTCGTGAAGGTGTAAGGTACTTTGTTGATCATAACACAAG
	WWP1 AS	488	AGGCTGGGAAATTAGATATACTCGTGAAGGTGTAAGGTACTTTGTTGATCATAACACAAG
20	WWP1 ORF	1560	AACAACAACATTCAAAGATCCTCGCAATGGGAAGTCATCTGTAATAAAGGTGGTCCACA
	WWP1 AS	548	AACAACAACATTCAAAGATCCTCGCAATGGGAAGTCATCTG-NACTAAAGG-GGTCCACA
	WWP1 ORF	1620	AATTGCTTATGAACGCGGCTTAGGTGGAAGCTTGCTCACTTCCGTTATTTGTGCCAGTC
25	WWP1 AS	606	AA-TGCTTA-NAACGCGGCGG-----
	WWP1 ORF	1680	TAATGCACTACCTAGTCATGTAAGATCAATGTGTCCCGGCAGACATTGTTTGAAGATTC
	WWP1 AS	624	-----
	WWP1 ORF	1740	CTTCCAACAGATTATGGCATTAAAACCTATGACTTGAGGAGGCGCTTATATGTAATATT
30	WWP1 AS	624	-----
	WWP1 ORF	1800	TAGAGGAGAAGAAGGACTTGATTATGGTGGCCTAGCGAGAGAATGGTTTTTCTTGCTTTC
	WWP1 AS	624	-----
35	WWP1 ORF	1860	ACATGAAGTTTTGAACCCAATGTATTGCTTATTTGAGTATGCGGGCAAGAACAATATTG
	WWP1 AS	624	-----
	WWP1 ORF	1920	TCTGCAGATAAATCCAGCATCAACCATTAAATCCAGACCATCTTTCATACTTCTGTTTCAT
40	WWP1 AS	624	-----
	WWP1 ORF	1980	TGGTCGTTTTATTGCCATGGCACTATTTTCATGGAAAGTTTATCGATACTGGTTTCTCTTT
	WWP1 AS	624	-----
	WWP1 ORF	2040	ACCATTCTACAAGCGTATGTTAAGTAAAAAATTACTATTAAGGATTTGGAATCTATTGA
45	WWP1 AS	624	-----
	WWP1 ORF	2100	TACTGAATTTTATAACTCCCTTATCTGGATAAGAGATAACAACATTGAAGAATGTGGCTT
	WWP1 AS	624	-----
50	WWP1 ORF	2160	AGAAATGTACTTTTCTGTTGACATGGAGATTTTGGGAAAAGTTACTTCACATGACCTGAA
	WWP1 AS	624	-----
	WWP1 ORF	2220	GTTGGGAGGTTCCAATATTCTGGTGAAGGAGAGACAAAGATGAATATATTGGTTTAAT
55	WWP1 AS	624	-----
	WWP1 ORF	2280	GACAGAATGGCGTTTTTCTCGAGGAGTACAAGAACAGACCAAAGCTTTCCTTGATGGTTT
	WWP1 AS	624	-----
	WWP1 ORF	2340	TAATGAAGTTGTTCTCTTTCAGTGGCTACAGTACTTCGATGAAAAAGAATTAGAGGTTAT
60	WWP1 AS	624	-----
	WWP1 ORF	2400	GTTGTGTGGCATGCAGGAGGTTGACTTGGCAGATTGGCAGAGAAATACTGTTTATCGACA
	WWP1 AS	624	-----
65	WWP1 ORF	2460	TTATACAAGAAACAGCAAGCAAATCATTTGGTTTTGGCAGTTTGTGAAAGAGACAGACAA

WWP1 AS 624 -----
WWP1 ORF 2520 TGAAGTAAGAATGCGACTATTGCAGTTCGTCACCTGGAACCTGCCGTTTACCTCTAGGAGG
WWP1 AS 624 -----
5 WWP1 ORF 2580 ATTTGCTGAGCTCATGGGAAGTAATGGGCCTCAAAAGTTTTGCATTGAAAAAGTTGGCAA
WWP1 AS 624 -----
10 WWP1 ORF 2640 AGACACTTGGTTACCAAGAAGCCATACATGTTTTAATCGCTTGGATCTACCACCATATAA
WWP1 AS 624 -----
WWP1 ORF 2700 GAGTTATGAACAACATAAGGAAAACTTCTTTTGCAATAGAAGAGACAGAGGGATTGG
WWP1 AS 624 -----
15 WWP1 ORF 2760 ACAAGAAGATTACAAGGACGACGACGATAAGTGA
WWP1 AS 624 -----

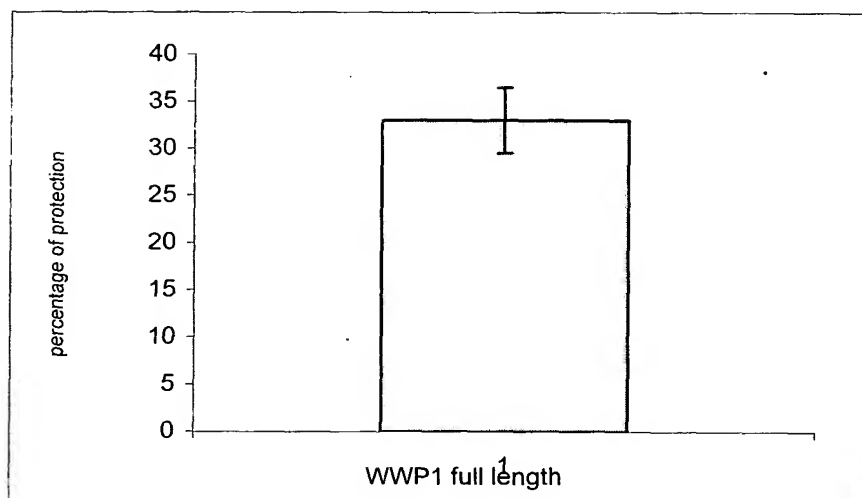
Figure 4:
validation of the anti-apoptotic effect of WWP1

a)

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b)



10